

9/7/07
311

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"20060014218".pn.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:41
L2	979	(golz.in. and (stefan.in. or s.in.)).	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:41
L3	161	(bruggemeier.in. and (ulf.in. or u.in.))	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:41
L4	115	(weingartner.in. and (bernhard.in. or b.in.))	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:42
L5	1099	I2 or I3 or I4	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:42
L6	6	I5 and npff\$4	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:42
L7	6	npffr1 or npff1r	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:42

EAST Search History

L8	11	flj10751	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:42
L9	0	gpr147	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:43
L10	0	gpcr147	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:43
L11	0	npff1r1	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:43
L12	22	ot7t022	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:43
L13	9	RFamide near5 related near5 peptide near5 receptor	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:44
L14	10	RFamide near15 related near15 peptide near15 receptor	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:44

EAST Search History

L15	45	I7 or I8 or I12 or I14	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:44
L16	1	I15 and I5	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:45
L17	35	I15 and (cardio\$10 or vascul\$10 or heart\$10 or myocard\$10 or ischem\$10)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:45
L18	1	I15 same (cardio\$10 or vascul\$10 or heart\$10 or myocard\$10 or ischem\$10)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:46
L19	2	"6262246".pn.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:47
L20	8	"2269192".pn.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/09/07 19:47

STN SEARCH HISTORY

9/7/07

34

=> d his

(FILE 'HOME' ENTERED AT 19:28:32 ON 07 SEP 2007)

FILE 'MEDLINE, EMBASE, BIOSIS, SCISEARCH, DISSABS, TOXCENTER' ENTERED AT 19:28:49 ON 07 SEP 2007

L1 478 S (GOLZ S?/AU) OR (BRUGGMEIER U?/AU) OR (WEINGARTNER B?/AU)
L2 3 S NPFFR1
L3 0 S GPR147
L4 0 S GPCR147
L5 0 S FLJ10751
L6 18 S OT7T022
L7 129 S RFAMIDE (1A) RELATED (1A) PEPTIDE
L8 3 S RFAMIDE (1A) RELATED (1A) PEPTIDE (1A) RECEPTOR
L9 23 S RFAMIDE (1A) RELATED (1A) PEPTIDE (5A) RECEPTOR
L10 9 DUP REM L6 (9 DUPLICATES REMOVED)
L11 71 S NPFF1
L12 0 S NPFF1R
L13 103 S L2 OR L6 OR L9 OR L11
L14 46 DUP REM L13 (57 DUPLICATES REMOVED)
L15 17 S L14 AND PY<=2002
L16 17 DUP REM L15 (0 DUPLICATES REMOVED)
L17 0 S L14 AND L1
L18 0 S L1 AND NPFF?
L19 2 S L14 AND (CARDIO?)
L20 0 S L14 AND (HEART OR MYOCARD? OR ISCHEM?)
L21 1 S L14 AND VASCUL?

=> log y

Sequence
Alignment #1

```
<!--StartFragment-->RESULT 1
NPFF1_HUMAN
ID NPFF1_HUMAN STANDARD; PRT; 430 AA.
AC Q9GZQ6; Q8NGR0; Q96RN3;
DT 27-APR-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 27-JUN-2006, entry version 38.
DE Neuropeptide FF receptor 1 (G-protein coupled receptor 147) (RFamide-
DE related peptide receptor OT7T022).
GN Name=NPFFR1; Synonyms=GPR147, NPFF1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spinal cord;
RX MEDLINE=20564301; PubMed=11024015; DOI=10.1074/jbc.M004385200;
RA Bonini J.A., Jones K.A., Adham N., Forray C., Artymyshyn R.,
RA Durkin M.M., Smith K.E., Tamm J.A., Boteju L.W., Lakhiani P.P.,
RA Raddatz R., Yao W.-J., Ogozalek K.L., Boyle N., Kouranova E.V.,
RA Quan Y., Vaysse P.J., Wetzel J.M., Branchek T.A., Gerald C.,
RA Borowsky B.;
RT "Identification and characterization of two G protein-coupled
RT receptors for neuropeptide FF.";
RL J. Biol. Chem. 275:39324-39331(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20482175; PubMed=11025660; DOI=10.1038/35036326;
RA Hinuma S., Shintani Y., Fukusumi S., Iijima N., Matsumoto Y.,
RA Hosoya M., Fujii R., Watanabe T., Kikuchi K., Terao Y., Yano T.,
RA Yamamoto T., Kawamata Y., Habata Y., Asada M., Kitada C., Kurokawa T.,
RA Onda H., Nishimura O., Tanaka M., Iyata Y., Fujino M.;
RT "New neuropeptides containing carboxy-terminal RFamide and their
RT receptor in mammals.";
RL Nat. Cell Biol. 2:703-708(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Liu Q., Guan X.-M., McDonald T.P., Jiang Q., Zeng Z., Marlene J.,
RA Williams D.L. Jr., Hong Y., Figueroa D., Clements M.K., Mallee J.,
RA Wang R., Evans J., Gould R., Austin C.P.;
RT "Identification and characterization of two cognate receptors for
RT mammalian FMRFamide-like neuropeptides.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for NPAF (A-18-F-amide) and NPFF (F-8-F-amide)
CC neuropeptides, also known as morphine-modulating peptides. Can
CC also be activated by a variety of naturally occurring or synthetic
CC FMRF-amide like ligands. This receptor mediates its action by
CC association with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF268898; AAG41397.1; -; mRNA.
DR EMBL; AB040104; BAB17677.1; -; mRNA.
DR EMBL; AF330055; AAK94199.1; -; mRNA.
DR EMBL; AB065729; BAC05950.1; ALT_SEQ; Genomic_DNA.
DR UniGene; Hs.302026; -.
DR Ensembl; ENSG00000148734; Homo sapiens.
DR HGNC; HGNC:17425; NPFFR1.
DR MIM; 607448; gene.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; NAS.
DR GO; GO:0008188; F:neuropeptide receptor activity; NAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR005395; NPFF_rcpt.
DR InterPro; IPR005396; NPFF_rcpt_1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRRHODOPSN.
DR PRINTS; PRO1570; NPFFRECEPTOR.
DR PRINTS; PRO1571; NPFFRECEPTR1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW Transducer; Transmembrane.
FT CHAIN 1 430 Neuropeptide FF receptor 1.
FT /FTId=PRO_0000069913.
FT TOPO_DOM 1 43 Extracellular (Potential).
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FT	TRANSMEM	44	64	1 (Potential).
FT	TOPO_DOM	65	80	Cytoplasmic (Potential).
FT	TRANSMEM	81	101	2 (Potential).
FT	TOPO_DOM	102	117	Extracellular (Potential).
FT	TRANSMEM	118	138	3 (Potential).
FT	TOPO_DOM	139	158	Cytoplasmic (Potential).
FT	TRANSMEM	159	179	4 (Potential).
FT	TOPO_DOM	180	214	Extracellular (Potential).
FT	TRANSMEM	215	235	5 (Potential).
FT	TOPO_DOM	236	271	Cytoplasmic (Potential).
FT	TRANSMEM	272	292	6 (Potential).
FT	TOPO_DOM	293	307	Extracellular (Potential).
FT	TRANSMEM	308	328	7 (Potential).
FT	TOPO_DOM	329	430	Cytoplasmic (Potential).
FT	CARBOHYD	10	10	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	18	18	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	29	29	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	113	113	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	195	195	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	116	203	By similarity.
FT	CONFLICT	376	376	V -> A (in Ref. 3).
SQ	SEQUENCE	430 AA;	47819 MW;	BBB0146281B2B9A0 CRC64;

Query Match 100.0%; Score 2278; DB 1; Length 430;

Best Local Similarity 100.0%; Pred. No. 1.4e-153;

Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVG 60
        |||
Db      1 MEGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVG 60

Qy      61 NTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMSG 120
        |||
Db      61 NTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMSG 120

Qy      121 LVQGMVSASVSFTLVIAIAVERFRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTL 180
        |||
Db      121 LVQGMVSASVSFTLVIAIAVERFRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTL 180

Qy      181 TVTREEHHFMDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIA 240
        |||
Db      181 TVTREEHHFMDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIA 240

Qy      241 RKLQAPGPAPGGEEAADPRASRRRRVHVHMLVMVALFFTLWLPLWALLLLIDYGQLSA 300
        |||
Db      241 RKLQAPGPAPGGEEAADPRASRRRRVHVHMLVMVALFFTLWLPLWALLLLIDYGQLSA 300

Qy      301 PQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAY 360
        |||
Db      301 PQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAY 360

Qy      361 SERPGGLLHRRVFVVVRPSDSGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSH 420
        |||
Db      361 SERPGGLLHRRVFVVVRPSDSGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSH 420

Qy      421 LPLTIPAWDI 430
        |||
Db      421 LPLTIPAWDI 430
<!--EndFragment-->

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